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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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UG-09-462-569B-4/C
; Sequence 4, Application US/09462569B
; Patent No. 6392124
; GENERAL INFORMATION:
APPLICANT: PORZ ASCASO, Fernando
APPLICANT: TORRES PASCUAL, Vicente
APPLICANT: TORRES PASCUAL, Vicente
TITLE OF INVENTION: THE TURNIP MOSAIC VIRUS (TuMV)
TITLE OF INVENTION: THE TURNIP MOSAIC VIRUS (TuMV)
TITLE OF INVENTION: THE TURNIP MOSAIC VIRUS (TuMV)
TITLE OF INVENTION UNMBER: US/09/462,569B
CURRENT FILING DATE: 2000-04-03
PRIOR PILING DATE: 1998-07-09
PRIOR PILING DATE: 1998-07-09
PRIOR PILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Artificial Sequence
FEATURE:
CURRENT NFORMATION: CONSTRUCT
CONTREMENT:
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US-08-381-572-20
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US-08-442-745-5
US-08-443-129-5
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PCT-US95-04467-5
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Pred. No. 0.0002;
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US-08-113-646A-44
; Sequence 44, Application US/08113646A
; Patent No. 5578468
; GENERAL INFORMATION:
; APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
; APPLICANT: ANTCZAK, James B.
; TITLE OF INVENTION: SITE-SPECIFIC RNA CLI
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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Best Local Similarity 100
Matches 32; Conservative
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ADDRESSEE: Behring Diagnostics GmbH, c/o Dade Behring Inc
STREET: 1717 Deerfield Road
CITY: Deerfield
STATE: Illinois
                                                                                                                                                                                                                                                                                                                    Homogeneous Amplification and Detection of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60015-0778

ZIP: 60015-0778

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 0.0002;
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                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,624B
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,090
                                                                                                                                                               Sequence 1, Application US/08771624B; Patent No. 5914230; GENERAL INFORMATION:
APPLICANT: Liu, Yen Ping
APPLICANT: Fatel, Rajesh D.
APPLICANT: Kurn, Nurith
APPLICANT: Lin, Claire
APPLICANT: Uin, Claire
APPLICANT: Uin, Claire
TITLE OF INVENTION: Homogeneous Amp
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NAME: Ruszala, Lois K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: 1030
TELECOMMUNICATION INFORMATION:
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SEQ ID NO:
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IDNESS: single
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CLASSIFICATION:
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US-08-440-209-4/c
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APPLICANT: TAIRA, KAZUNARI
APPLICANT: MATSUZAKI, JUNICHI
APPLICANT: OHMORI, HIROSHI
TITLE OF INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH
TITLE OF INVENTION: ITS USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No. 0.0002;
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                                                                                                                                                     Version
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CURRENT APPLICATION NUMBER: US/09/720,201A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: JP 98/177,820
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/113,646A FILING DATE: 31-AUG-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/084,406 FILING DATE: 10-AUG-1987 ATTORNEY/AGENT INFORMATION:
                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                      32,955
R: 1579-20
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    : 1100 NORTH GLEBE ROAD ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA (genomic)
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Best Local Similarity 100.0%;
Matches 32; Conservative (
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ORGANISM: Artificial Sequence
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(703) 816-4100
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                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                   NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MICHINORI
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                   SOFTWARE: Patentin Re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 22201-4714
                                      VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOHARA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-113-646A-44
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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ENGTH: 38
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APPLICANT:
APPLICANT:
APPLICANT:
      STREET:
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LENGTH:

Length 40;

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Version
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Pred. No.
                                                                                                                                                                                                                                                                                  29,809
R: C0772/7004
                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,996
FILING DATE:
                                                                                                                                                                                     US/08/477,895A
                                                                                                                        US/08/439,996
                                                                                                                                                                                                                     US 08/128,583
                                                                                                                                                                                                                                                               NAME: Janiuk, Anthony J
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C077
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09732067
Patent No. 6457426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Sc.
100.0%; Pr
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                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE:
APPLICATION NUMBER: US 08/
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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nucleic acid
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Best Local Similarity 100.
Matches 32; Conservative
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Best Local Similarity
Matches 32; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
TYPE: n
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Patent No. 6057093

GENERAL INFORMATION:

APPLICANT: Han, Jang H

APPLICANT: Spaete, Richard R

TITLE OF INVENTION: Methods and Compositions for Controlling

TITLE OF INVENTION: Translation of HCV Proteins

NUMBER OF SEQUENCES: 5
                                                                                                        Controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,209
FILING DATE: 12-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/477,895
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/128,583
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J
REGISTRATION NUMBER: 29,809
                                                                                                      Compositions for of HCV Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 2; Lost Pred. No. 0.0002; D; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: C0772/7004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
GENERAL INFORMATION:
APPLICANT: Han, Jang H
APPLICANT: Spaete, Richard R
TITLE OF INVENTION: Methods and Co
TITLE OF INVENTION: Translation of
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, and
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                     and
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100.0%; P.
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1: 600 Atlantic Avenue
Boston
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32; Conservative
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nucleic acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Green STREET: 600 Atlantic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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.08-439-996-4/c
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US-08-440-209-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Best Local
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US-08-4
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DB 3; Lc. 0.0002; 0;

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                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ullman, Edwin
APPLICANT: Singh, Rajendra
APPLICANT: DeKeczer, Steve
APPLICANT: Davalian, Dariush
TITLE OF INVENTION: Amplified Luminescent Homogeneous
TITLE OF INVENTION: Immunoassay
FILE REFERENCE: BEH-7385
CURRENT APPLICATION NUMBER: US/09/732,067
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 4; Le
Pred. No. 0.0002;
0; Mismatches 0;
2098
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                        ; OTHER INFORMATION: hybridization oligo US-09-732-067-7
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Gaps

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Length 41;
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Length 50;
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0.0002;
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Score 32; DB 4; Lo
Pred. No. 0.0002;
); Mismatches 0;
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Pred. No. 0.00055
); Mismatches 0
                                                                 2098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-197-814-9/c
is Sequence 9, Application US/09197814A
j Patent No. 6316220
j GENERAL INFORMATION:
i TITLE OF INVENTION:
i TITLE OF INVENTION:
i TITLE OF INVENTION:
i CURRENT APPLICATION NUMBER: US/09/197,814A
i CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 0740/96
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1997-07-07
NUMBER OF SEQ ID NOS: 14
software: FastSEQ for Windows Version 3.0
                                                                                                 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human F.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14715
LENGTH: 50
                                                                                    2067 AAAAAAAAAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                 Human
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Pred. No.
                                                                                                                                                                   Sequence 14715, Application US/09621976
Sequence 14715, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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th 1.5%; Somilarity 100.0%; 132; Conservative 0;
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ORGANISM: Artificial
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31; Conserv
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32; Conser
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Best Local S
Matches 31
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                                                                   2067
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US-09-621-976-14612

Sequence 14612, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 14612

LENGTH: 50
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                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/420,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Patent No. 5607834
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Bruce Bagwell
TITLE OF INVENTION: NUCLEIC ACID PROBES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Y. ROCKY TSAO
REGISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 05663/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   us/01/990,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred
                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 19921210
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 32; Conser
                                                                                                                                                                                   STREET: 225 F. CITY: Boston STATE: Massacl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-420-443-1
                      US-08-420-443-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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         RESULT 8
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ORGANISM: Homo

TYPE: DNA

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TOPOLOGY: 1:
MOLECULE TYPE:
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US-09-165-239A-5/C
; Sequence 5, Application US/09165239A
; Patent No. 6344554
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, ALEXANDER
; APPLICANT: DEAUN, BURKHARD R
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES FROM CANDIDA
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: 220022000700
; CURRENT APPLICATION NUMBER: US/09/165,239A
; CURRENT APPLICATION NUMBER: US/09/165,239A
; CURRENT PILING DATE: 1998-10-01
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASELSEQ for Windows Version 3.0
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Mismatches 0;
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Sequence 9, Application US/09920581

Patent No. 6555657

GENERAL INFORMATION:

APPLICANT: Christensen, Tove

TITLE OF INVENTION: A Transcription Factor

FILE REFERENCE: 4484.204-US

CURRENT APPLICATION NUMBER: US/09/920,581

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 09/197,814

PRIOR FILING DATE: 1998-11-23

PRIOR FILING DATE: 1997-07-07

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Recie, Lisa
APPLICANT: Merberg, David
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100.0%; Pr
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0%;
Matches 31; Conservative (
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Best Local Similarity
Matches 31; Conser
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,596B
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
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red. No. 0.00055;
Mismatches 0;
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Patent No. 6642361;
GENERAL INFORMATION:
APPLICANT: Hunter, Fiona F.
TITLE OF INVENTION: Isolated Cocoon Silk Profit TITLE OF INVENTION: Encoding Such Protein FILE REFERENCE: 1468-001A;
CURRENT APPLICATION NUMBER: US/09/894,916;
CURRENT FILING DATE: 2001-06-28;
PRIOR FILING DATE: 2000-06-29;
NUMBER OF SEQ ID NOS: 7;
SOFTWARE: Patentin version 3.1
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CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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100.0%;
         Evans, Cheryl
Spaulding, Vikki
Bowman, Michael
Maurice
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TYPE: DNA
ORGANISM: Simulium vittatum
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nucleic acid
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NAME/KEY: misc_feature
LOCATION: (44)...(45)
OTHER INFORMATION: n can
          APPLICANT: Evans, Che
APPLICANT: Spaulding,
APPLICANT: Bowman, Mi
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STREET: 87 Cambr.
CITY: Cambridge
STATE: Massachus
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Best Local Similarity
Matches 31; Conser
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1.5%; Score 31; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 31; Conservative 0; Mismatches 0; Indels

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Search completed: July 2, 2004, 07:38:41 Job time : 158 secs

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US-09-827-289-22
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155 32 1.5 1.6 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5	-10-463-549-2	-10-218-567-7	-10-352-253A-3	-09-764-891-1017	-10-289-921-5	-10-062-188-1	-10-668-749A-	-09-815-343-101	S-10-097-105-101	-09-920-581-	S-10-371-421-	-09-932-165-148	-09-942-052-71	-10-013-312-299	-10-087-190-3	S-10-121-019-1	S-10-120-885A-2	-10-121-016-5	-10-114-669-6	-10-114-432-4	-09-894-916-	-09-880-727-1	-10-314-578-109	-10-314-578-109	-10-042-193A	-10-042-193A-	-10-380-584-11	-10-371-600-	-10-371-600-	-10-219-195-2	-10-219-195-2
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## ALIGNMENTS

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Sequence 4651, Application US/10131827
Sequence 4651, Application US/10131827
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Sequence 4651, Application US/2004000947941
Sequence 4651, Application No. US2004000947941
Settle Carry Woodward, Day
APPLICANT: Woodward, Robert
APPLICANT: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-10-22
PRIOR PAPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin Version 3.1
LENGTH: 50
TYPE: DNA
NORGANISM: Homo
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US-09-827-289-14/c

RESULT

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Sequence 14, Appiron.

Sequence 14, Appiron.

Batent No. US20020009716A1

GENERAL INFORMATION:

APPLICANT: Abarzua, Patricio

TITLE OF INVENTION: Extension

FILE REFERENCE: 469290-55

CURRENT APPLICATION NUMBER: US/09/827,289

CURRENT FILING DATE: 2001-04-05

PRIOR FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension
FILE REFERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: use in allele discrimination
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OTHER INFORMATION: use in allele discrimination
9-827-289-14
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Pred. No. 4.3
0; Mismatches
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Patent No. US20020009716A1
GENERAL INFORMATION:
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Best Local Similarity 100.
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ORGANISM: Artificial
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Best Local Similarity
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LENGTH: 45
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RESULT 5
US-09-827-289-25/c
is-o9-827-289-25/c
j Sequence 25, Application US/09827289
j Patent No. US20020009716Al
j GENERAL INFORMATION:
i APPLICANT: Abarzua, Patricio
i TITLE OF INVENTION: Extension
i FILE REFERENCE: 469290-55
j CURRENT FILING DATE: 2001-04-05
j PRIOR APPLICATION NUMBER: U.S. 60/194843
j PRIOR FILING DATE: 2000-04-05
j NUMBER OF SEQ ID NOS: 35
software: Patentin Ver. 2.1
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CTHER INFORMATION: use in allele discrimination
US-09-827-289-25
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Pred. No. 4.3e-06,
; Mismatches 0
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APPLICANT: Hong, Zhi
APPLICANT: Hong, Zhi
APPLICANT: Ferrari, Eric
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REFERENCE: IN01165
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: U.S. 60/195,852
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 46
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Patent No. US20020064771A1
GENERAL INFORMATION:
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100.0%; Pr
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Best Local Similarity 100.0%;
Matches 34; Conservative (
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ORGANISM: Artificial
FEATURE:
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Best Local Similarity
Matches 34; Conser
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Allele Discrimination

Sequence 21, Application US/09827289 Patent No. US20020009716A1 GENERAL INFORMATION:

US-09-827-289-21/c

APPLICANT: Abarzua, Patricio TITLE OF INVENTION: Process for TITLE OF INVENTION: Extension FILE REFERENCE: 469290-55

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Best Local Similarity 100
Matches 32; Conservative
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Matches 33; Conser
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Best Local Similarity
Matches 33; Conser
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COTHER INFORMATION:
US-09-827-289-26
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Sequence 22, Application US/09827289

Sequence 22, Application US20020009716A1

GENERAL INFORMATION:

APPLICANT: Abarzua, Patricio

TITLE OF INVENTION: Extension

FILE REFERENCE: 469290-55

CURRENT APPLICATION NUMBER: US/09/827,289

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: U.S. 60/194843

PRIOR FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1
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                                                                   Sequence:
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Pred. No. 1.3e-05;
0; Mismatches 0;
                                                                                                              Score 33; DB 9; L. Pred. No. 1.3e-05; 0; Mismatches 0;
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                                                 FEATURE: OTHER INFORMATION: Description of Artificial
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TITLE OF INVENTION: HCV REPLICASE COMPLEXI
FILE REFERENCE: IN01165
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: U.S. 60/195,852
PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09828034
Patent No. US20020064771A1
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100.0%; Pr
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larity 100.0%; P
Conservative 0;
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2000-04-06
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                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2
                                                                                                   Query Match
Best Local Similarity
LENGTH: 36
TYPE: RNA
ORGANISM: Artificial
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US-09-828-034-3
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US-09-828-034-2
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LENGTH: 46
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; Sequence 2, Application US/10371600
; Publication No. US20030180776A1
; GENERAL INFORMATION:
; APPLICANT: WU, MING
; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION
; FILE REFERENCE: 3817.10-2
; CURRENT APPLICATION NUMBER: US/10/371,600
; CURRENT APPLICATION NUMBER: 60/359,223
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
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 Length 46;
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Pred. No. 1.4e-05;
); Mismatches 0;
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Pred. No. 4.2e-05;
0; Mismatches 0;
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Pred. No. 1.4e
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                                                                                                        38 САВАВАВАВАВАВАВАВАВАВАВАВАВАВАВАВ
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TITLE OF INVENTION: Process for Allele Discr
TITLE OF INVENTION: Extension
FILE REFERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 46
                                                                                                                                                                                          Sequence 26, Application US/09827289
Patent No. US20020009716A1
GENERAL INFORMATION:
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100.0%; Pi
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100.0%; Pi
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LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local S
Matches 32
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Matches 32
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                                         US-09-764-891
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APPLICANT: ULLMAN, EDWIN F.
TITLE OF INVENTION: DETECTION BY SLIDING 1
FILE REFERENCE: 3817.10-2
CURRENT APPLICATION NUMBER: US/10/371,600
CURRENT FILING DATE: 2003-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/371,600 CURRENT FILING DATE: 2003-05-19 PRIOR APPLICATION NUMBER: 60/359,223 PRIOR FILING DATE: 2002-02-20
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APPLICATION NUMBER: 60/379,360
FILING DATE: 2002-05-08
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OTHER INFORMATION: oligonucleotide
0-371-600-10
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                                                                                             Sequence 9, Application US/10371600 Publication No. US20030180776A1 GENERAL INFORMATION:
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APPLICANT: ULLMAN, EDWIN F.
TITLE OF INVENTION: DETECTION BY
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PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/37
PRIOR FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
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SOFTWARE: PatentIn Ver.
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; Sequence 6, Application US/10289921
; Publication No. US20030113337A1
; GENERAL INFORMATION:
; APPLICANT: MERUELO, Daniel
; APPLICANT: OHNO, Kouichi
; APPLICANT: LEVIN, Brandi A.
; TITLE OF INVENTION: HIGH EFFICIENCY TISSUE S;
; TITLE OF INVENTION: DELIVERY SYSTEM USING S;
; FILE REFERENCE: 5986/11123-US1
; CURRENT APPLICATION NUMBER: US/10/289,921
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 08/566,421
; PRIOR FILING DATE: 1995-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10175
LENGTH: 38
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Publication No. US20040053308A1
GENERAL INFORMATION:
APPLICANT: Nakamura, Kumi
TITLE OF INVENTION: Probe Immobilized 8
TITLE OF INVENTION: Analytical Method
FILE REFERENCE: 03560.003309
S-09-764-891-10175
Sequence 10175, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, ProFILE REFERENCE: PC006
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Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., C. Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, I mapping of mRNA start sites  EMBO Rep. 2 (5), 388-393 (2001)	Contact: Yutaka Suzuki Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,
AUTHORS TITLE JOURNAL MEDLINE	COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A.
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01421"
/clone_lib="Sugano Homo s
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/mol_type="mRNA"
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CAS01421, mRNA sequence.
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larity 100.0%;
Conservative (
   Sugano, S. Construction
length-enriched and a
149-156 (1997).
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AU106825
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EST 30-AUG-2001

linear

cDNA clone

AU106826 Sugano Homo sapiens cDNA library Homo sapiens

DEFINITION

AU106826 LOCUS

RESULT

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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.,

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CLone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 203 Std Error: 0.00

Seg primer: -40ml3 fwd. ET from Amersham.
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AA564185
AA564185.1 GI:2335824
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1 (bases 1 to 50)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                Euteleostomi;
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072
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                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A.
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene
149-156 (1997).
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS03470"
/clone_lib="Sugano Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens"
GI:13556347
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|larity 100.0%;
|Conservative (
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                                                   (human)
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Query Match
Best Local Similarity
Matches 33; Conser
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BU431798/c
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                                                                                                      /tissue_type="normal prostate"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr21"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is not normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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/dev_stage="proliferated callus on 2N6 media for 30 days'
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Division
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacea
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 40)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GreenGene Biotech Inc.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shi Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shi Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Genomics and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF332441
NACL--08-P05.b1 Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--08-P05, mRNA sequence.
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Pred. No. 0;
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                               sapiens"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-P05"
                                            mol_type="mRNA"
|db_xref="taxon:9606"
|clone="IMAGE:985365"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
                               /organism="Homo
                                                                                                                                                                                                                                                                                                       1.7%; Sc.
100.0%; P<sub>1</sub>
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100.0%; P<sub>1</sub>
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                                                                                           sex="male"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

"I (bases 1 to 33)

"NIH-MGC http://mgc.nci.nih.gov/.

"National Institutes of Health, Mammalian Gene Collection (MGC)

"In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/.

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Location/Qualifiers

1. .33

High quality sequence stop: 31.

Location/Qualifiers

1. .33

Mol. type="MRNA"

Abost="MRNA"

Abost="MRNA"

Lissue_type="MRNA"

Abost="MRNA"

Lissue_type="MRNA"

Abost="MRNA"

All: Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.8 kb. Library constructed by Life

Technologies. "

Technologies."
                                                                                                                            33 bp mRNA linear EST 09-SEP-2002 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855694 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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601655967R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855737 3',
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No.
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100.0%; P.
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BU431798
BU431798.1 GI
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BU431799
BU431799.1 GI
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601655890R1
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Gaps

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Indels

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 $^{\circ}$ 

Length

14;

DB 0;

(from clone DKFZp564E1872)

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CDNA

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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available at the RZPD in Berlin
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF302212
7LEAF--07-I14.bl Rice leaf plasmid cDNA library II sativa cDNA clone 7LEAF--07-I14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gassenhuber J., Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ted (12-MAR-1999) to the EMBL/GenBank/DDBJ datab
Am Klopferspitz 18a D-82152 Martinsried, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from S. Wiemann, sequenced by LMU within the scing consortium of the German Genome Project sequence available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:9606"
/mol_type="mRNA"
/organism="Homo sapiens"
/clone="DKFZp564E1872"
/clone_lib="564 (synonym: hfbr2).
Xl-2blue; sites NotI + SalI"
/dev_stage="fetal"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                          Version 1)
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                                                                            Mismatches
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Pred. No.
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                                              Score 33;
Pred, No.
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Last updated,
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/db
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12-MAR-1999
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                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3855737"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           racheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza
Contact: Robert StrausDels, ---
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can bi
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM570 row: e column: 18
High quality sequence stop: 31.
Location/Qualifiers
1. .34
1. .34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Liliopsida; Embryophyta; Trac)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.;
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA linear EST CDNA library (NACL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Rice callus plasmid cDNA library /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA with oligoribonucleotides and then used as te
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue type="callus"
dev stage="proliferated callus on 2N6 media"
lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bhnahm@bio.myongji.ac.kr
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                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF327755

NACL--02-F23.bl Rice callus plasmid cDNA libra: sativa cDNA clone NACL--02-F23, mRNA sequence. CF327755
CF327755.1 GI:33803761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--02-F23"
                                                                                                                                                                                                                                                                                                                                                                                                             Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bhnahm@ggbio.com, bhn
Location/Qualifiers
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EST 15-AUG-2003 (7LEAF) Oryza

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Length

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ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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KEYWORDS

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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--03-K14"
/tissue_type="leaf"
/tissue_type="leaf"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enic rice plasmid cDNA -03-K14, mRNA sequence.
                                                                                                                                                                                                                  and then used for PCR."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryza.

I (bases 1 to 44)
S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Dividence and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
                                                                                                                                                                                                  EcoRI; Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMT--03-K14.bl AtJMT-overexpressing transgenic rice library (JMT) Oryza sativa cDNA clone JMT--03-K14, m CF334384
CF334384.1 GI:33817097
EST.
                                                                                                                                                          plasmid
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                                                                                                              germination"
                                                                                                        'dev_stage="14 days after germinati
'lab_host="E.coli DH10B"
'clone_lib="Rice cold treated leaf
                                                                                                                                                                                           /note="Vector: pCR4-TOPO; Site 1:
incubated at 4 C(360uM/m-2sec-1) f
mRNA was reverse transcribed and t
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Oryza sativa"
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                           cultivar="Nackdong"
db_xref="taxon:4530"
clone="CLD1--01-M22"
                                                                                          tissue_type="leaf"
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100.0%; Pr
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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33; Conserv
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AUTHORS
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was capped
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                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryza.

1 (bases 1 to 44)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y. Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Divof Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryza.

Enthartoideae; Oryza.

Kim,J., Lee,T.H., Shin,Y.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Diversity

Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-114"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7)
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                                                                                                                                                                                                                                                                                                                          Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
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                       GI:33673973
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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RESULT 11 CF305473/c LOCUS

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TITLE JOURNAL COMMENT

REFERENCE AUTHORS

Tracheophyta;

Shin, Y.C.,

Division

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Gaps

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/mol_type="mRNA"
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/strain="FVB/N"
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/clone="IMAGE:4208373"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: this is a NCI_CGAP_Library."
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                                               BF582680
602094085F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208373 5',
mRNA sequence.
BF582680
BF582680.1 GI:11656398
BST.
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S. and Hall, N.
setse fly Glossina
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae, Murinae

Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae, Murinae

E 1 (bases 1 to 45)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MG

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed Boy: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9772 row: j column: 22

High quality sequence stop: 45.

Location/Qualifiers

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Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pte
Neoptera; Endopterygota; Diptera; Brachycera; Muscomor
Hippoboscoidea; Glossinidae; Glossina.
1 (bases 1 to 46)
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Oryza sativa

Oryza sativa

Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryza.

E 1 (bases; Lto 46)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Voncin. Kyeonggi, Korea
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/db_xref="taxon:4530"
/clone="NACL--08-120"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media fo
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (N
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NACL--08-I20.gl Rice callus plasmid cDNA library (NACL) sativa cDNA clone NACL--08-I20, mRNA sequence.
CF332152
CF332152.1 GI:33812528
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14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads staend of the cDNA all plc reads are from the 3' end.
                                                                                                                                                                                              Campus
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/organism="Glossina morsitans morsitans"
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/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse57d10_q1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans ad
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Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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/note="P1 primer for use in all
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10-JUL-2001
14-APR-1997 JP 1997537270
18-APR-1996 US 08/634325
KENNETH JACOBS, JOHN M MCCOY, LISA A RACIE, EDWARD R
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Process for allele discrimation utilizing primer
Process for allele discrimation utilizing primer
Patent: WO 0177390-A 26 18-OCT-2001;
Molecular Staging, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Pl primer for use in alla
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C12N15/12,C07K14/47,A61K38/17
Strandedness: Double;
Topology: Linear;
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db_xref="taxon:32644"
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Jacobs, K., Mccoy, J.M., Ra
Spaulding, V.
Secretory protein
Patent: JP 2001509004-A 1
GENETICS INSTITUTE INC
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JP 2001509004-A/14.
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                                                         www.ou/y2280-A/13.

synthetic construct
artificial sequences.

E 1 (bases 1 to 33)

Sato,S.

L Patent: WO 0079280-A 13 28-DEC-2000;

Datection kit for SRSV

L Patent: WO 0079280-A 13 28-DEC-2000;

JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE,MITSUAKI
MORIGUCHI,KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD,NAOKAZU
TAKEDA,KATSURO NATORI,TATSUO MIYAMURA, KUNIO KAMATA,TOSHINORI
SATO,SEIYA SATO
OS Artificial Sequence
BN WO 0079280-A/13
PD 28-DEC-2000
PF 22-JUN-1999 JP 99P 175928
PR SELYA SATO

C GOIN33/569,CI2N15/40
CC
FH Key Location/Qualifiers.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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THEIR USE
6 08-FEB-1996;
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Patent: US 6457426-A 7 01-OCT-2002;
Location/Qualifiers
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Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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7 from Patent WO0161033
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/mol_type="genomic DNA"
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from Patent WO9603528
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Petrik, J., Allain, J. a
OLIGONUCLEOTIDES AND T
Patent: WO 9603528-A 6
LYNXVALE LTD (GB)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct'
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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REFERENCE AUTHORS

JOURNAL

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AX225198.1

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84p2a9: a prostate and testis specific protein highly exprostate cancer
Patent: WO 0155391-A 7 02-AUG-2001;
Urogenesys, Inc. (US)
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Pred. No. 1.1e-05;
0; Mismatches 0;
                                                                                  Schouten, J. P.

Multiplex ligatable probe amplification
Patent: WO 0161033-A 7 23-AUG-2001;
Schouten, Johannes Petrus (NL)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

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    /organism="synthetic construct/mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="synthetic DNA"

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Copyright (c) 1993 - 2004 Compugen Ltd.	רבעים יה הביימי להשבמת מימוחות מימוחות MO"
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Search time 822 Seconds (without alignments) 10842.725 Million cell : 53 : 23 03 2004,  $^{\circ}$ July Run on:

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...aaaaaaaaaaaaaaaaaa ggccattatggatggatggg.... US-09-445-223-2 2098 score: Sequence: Title: Perfect

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residues 0. 9 Gapext OLIGO NUC Gapop 60.0

2124099041 3373863 seqs, Searched:

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## ALIGNMENTS

BP 50 entry) ABZ04660 standard; DNA; (first 09-JAN-2003 ABZ04660; RESULT 1 ABZ04660 

expression profiling probe SEQ ID NO 4651. Human leukocyte gene

T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; SS.

Homo sapiens

WO200257414-A2

25-JUL-2002

2001WO-US047856. 22-OCT-2001; 20-OCT-2000; 2000US-0241994P 08-JUN-2001; 2001US-0296764P

(BIOC-) BIOCARDIA INC

J, Phillips Prentice J, ., Altman P, , Johnson Wohlgemuth J, Fry K, Matcuk G, 1 Ly N, Woodward R, Quertermous T,

WPI; 2002-636525/68

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

English. dd<sub>0</sub> Claim 1; Page 476;

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient,

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predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
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discrimination Pl primer #12. ВР 45 (first entry) AAS95728 standard; DNA; 14-FEB-2002 Allele RESULT 2 AAS95728/c 

Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

sapiens. Homo

WO200177390-A2

18-OCT-2001.

2001WO-US011151 05-APR-2001; 05-APR-2000; 2000US-0194843P.

(MOLE-) MOLECULAR STAGING INC

ь, С Abarzua 2002-049157/06

to target target Detecting single nucleotide polymorphism involves amplifying t sequences using small primer probe that matches or mismatches sequence and extending primer probe which is then detected.

English 67pp; 41; Page Claim 15;

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target contacting an allele-specific oligonucleotide primer (P1) with a target sequence is complementary to P1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single nucleotide mismatch. Primer sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification amplification in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

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disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma a melanoma. Sequences AAS95711-AAS95745 represent primers, targets and fluorescence decorators used in the detection of RCA products
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AAS95724 standard; DNA; 45

(first entry)

14-FEB-2002

AAS95724;

Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe. discrimination P1 primer #8. (MOLE-) MOLECULAR STAGING INC 2000US-0194843P 2001WO-US011151 2002-049157/06 WO200177390-A2 05-APR-2001; 05-APR-2000; Homo sapiens 18-OCT-2001. Abarzua P; Allele WPI; 

Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

Claim 15; Page 41; 67pp; English

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (PI) with a target contacting an allele-specific oligonucleotide primer (PI) with a target sequence is complementary to PI at one end but the terminal nucleotide and the chird nucleotide from the terminal at the other end of PI may not be complementary. The complex is then contacted with an exonuclease complementary. The complex is then contacted with an exonuclease of the final polymerase enzyme under conditions that promote extension of PI with the target DNA as the template, thereby forming an extended segment of PI, Oligonucleotide probes hybridising to one or more target segment of PI, Oligonucleotide probes hybridising to one or more target colling tringuish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single nucleotide mismatch. Primer sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

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disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and melanoma. Sequences AAS95711-AAS95745 represent primers, targets and fluorescence decorators used in the detection of RCA products
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Gaps ö Length 45; Indels 0 2098 red. No. 0.0044; Mismatches 0 4 9 TGAAAAAAAAAAAAAAAAAAAAAAAAAAA TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA DB Score 34; Pred. No. .; 100.0%; 1.6%; Conservative Similarity 34; 37 2065 Query Match Best Local Matches d ਠੋ

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RESULT 4 AAS95735/c ID AAS95735 standard; DNA; 46

AAS95735;

(first entry) 14-FEB-2002 

Allele discrimination PI primer #19.

stomach; Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

Homo sapiens

WO200177390-A2

18-OCT-2001.

05-APR-2001; 2001WO-US011151

05-APR-2000; 2000US-0194843P.

(MOLE-) MOLECULAR STAGING INC

Abarzua

WPI; 2002-049157/06

target rget 0 ta a mismatches Detecting single nucleotide polymorphism involves amplifying sequences using small primer probe that matches or mismatches sequence and extending primer probe which is then detected.

Claim 15; Page 42; 67pp; English.

an extended more target 3' ends, hence sequence d the a single extension sequence on an amplification a target induced The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target sequence to form a hybridisation complex, where the target sequence to form a hybridisation complex, where the target sequence is complementary to P1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease complementary. The target DNA as the template, thereby forming an extended of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, he the absence of sequence amplification indicates the presence of a sing nucleotide mismatch. Primer sequences complementary to a sequence on a sequence of a sing and if in a time target on it is a sequence of a sing and if in a time target on it is a sequence of a sing and it is a sing a sequence of a se circle can be used in rolling circle amplification useful for diagnosing a disease caused by, inductation in at least one gene, such as Parkinson's kidney disease, Tay-Sachs disease, Huntington sms by not be disease, polycystic kidney disease, a mutation amplification target (RCA). The method is by or related to

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disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma a melanoma. Sequences AAS95711-AAS95745 represent primers, targets and fluorescence decorators used in the detection of RCA products
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AAS95731/c RESULT 5

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46 standard; DNA; AAS95731

AAS95731;

(first 14-FEB-2002

Allele discrimination P1 primer #15

Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

sapiens. Homo WO200177390-A2.

18-OCT-2001.

2001WO-US011151. 05-APR-2001;

05-APR-2000; 2000US-0194843P

(MOLE-) MOLECULAR STAGING INC

ď Abarzua WPI; 2002-049157/06.

target s to target Detecting single nucleotide polymorphism involves amplifying t sequences using small primer probe that matches or mismatches sequence and extending primer probe which is then detected.

15; Page 42; 67pp; English.

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target contacting an allele-specific oligonucleotide primer (P1) with a target polynucleotide to form a hybridisation complex, where the target sequence is complementary to P1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease deficient DNA polymerase enzyme under conditions that promote extension of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single nucleotide mismatch. Primer sequences complementary to a sequence on an electide mismatch. Primer sequences complementary to a sequence on an election target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington sednence hence

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virus (HCV) NS5B replicase RNA ВР 36 (first entry) ABK99273 standard; RNA; Hepatitis C 21-OCT-2002 **ABK99273** RESULT ABK9927 셤

synthesis template

ss; RNA polymerase.

replicase; NSSB 2001US-00828034 2000US-0195852P virus; HCV; ZHONG W. -A1 07-APR-2000; 06-APR-2001; US2002064771 U 30-MAY-2002 Synthetic. Hepatitis (ZHON/) 

Z HONG Z. FERRARI Hong Zhong W, (FERR/)

(HONG/)

comprising hepatitis C virus NS5B reg to which a 2 nucleotide-long primer which do not form a stable duplex in Ferrari Novel replicase complex c nucleotide-long template and template and primer w 2002-582330/62 WPI;

6; 17pp; English Example; Page

HCV NS5B.

of.

icity and he development mic constants The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NS5B replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NS5B protein. The complex is useful for detecting HCV replicase activity and permits establishment of sensitive RNA-dependent RNA polymerase assays to screen and evaluate antiviral inhibitors and to improve the specificity and efficacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of ACV NS5B-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mis-incorporation or chain termination. Specifically, the short RNA template and primer pairs are useful in screening assays which are used for determining kinetic, thermodynamic and mechanistic properties of NS5B replication and ultimately in the development of inhibitors of NS5B. Newly identified inhibitors of replicase activity may be used for developing anti-HCV pharmaceuticals. Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis

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                                                                                                                                                                                                                                                                     Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed and template and primer which do not form a stable duplex in the absence of HCV NS5B.
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                                                                                                              (first entry)
                        Conservative
                                                                                                                                       virus; HCV;
                                                                                    standard; RNA;
                                                                                                                                                                                                                                                             2002-582330/62
                   Similarity
                                                                                                                          virus
                                                                                                                                                                                                                                                Ŋ,
                                                                                                                                                                                                                     ZHONG W.
                                                                                                                                                                                                                                  FERRARI
                                                                                                                                                                  US2002064771-A1
                                                                                                                                                                                                                                                 Hong
                                                                                                                                                                                                         07-APR-2000;
                                                                                                                                                                                            06-APR-2001;
                                                                                                                                                                               30-MAY-2002.
                                                                                                                                       C
                                                                                                                           Ö
                                                                                                              21-OCT-2002
                         33;
                                                                                                                          Hepatitis
                                                                                                                                        Hepatitis
                                                                                                                                                    Synthetic
                                                                                                 ABK99272;
Sequence
                                                                                                                                                                                                                                                 Z,
                                                                                    ABK99272
                                      2066
            Query Match
Best Local
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                  Best Loc
Matches
                                                                       RESULT
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The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NS5B replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NS5B protein. The complex is useful for detecting HCV replicase activity and permits and evaluate antiviral inhibitors and to improve the specificity and esticacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NS5B-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mis-incorporation or chain termination.

Specifically, the short RNA template and primer pairs are useful in screening assays which are used for determining kinetic, thermodynamic contraction and investigation in the development screening assays which are used for determining kinetic, thermodynamic Specifically, che which are used for determining Kinchel, which are used for determining Kinchel, in the and mechanistic properties of NS5B replication and ultimately in the development of inhibitors of NS5B. Newly identified inhibitors of development of inhibitors of for developing anti-HCV pharmaceuticals. replicase activity may be used for developing anti-HCV pharmaceuticals replicase activity may be used for developing replicase RNA synthesis sequences emplates

6; 17pp; English

Example; Page

plicase, a 3 is annealed,

the absence

0 Other; ū; 0 Ë 0 .. G  $^{\circ}$ ü 0 Ą; 34 36 Sequence S

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                      Gaps
                     Ö,
       Length 36;
                     Indels
                   0;
    Pred. No. 0.011; ; Mismatches 0
                                         GAAAAAAAAAAAAAAAAAAAAAAAAAAAA
     Score
1.6%; Sc.
100.0%; Pi
                   Conservative
           Local Similarity
les 33; Conser
                                  2066
    Query Match
                  Matches
           Best
                                               엄
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AAD27116 standard; RNA; AAD271

BP

36

AAD27116;

(first entry) 09-APR-2002

to direct RNA synthesis by HCV RNA polymerase AA used template,

5B; NS5B; protein virus; HCV replicase; non-structural compound; RNA polymerase; ss. Hepatitis C lead

Unidentified.

US6322966-B1

27-NOV-2001

02960E00-SD66 11-MAY-1999;

99US-00309670 11-MAY-1999;

ZHONG W. (ZHON/)

HONG Z.

LAU JY N. (LAUJ/)

Lau JYN; Hong Z, Zhong W,

WPI; 2002-096587/13.

Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates, buffer

Example 1; Fig 1A; 10pp; English

The present invention relates to an assay system for hepatitis C virus (HCW) replicase activity. The assay system comprises an RNA template that has an unstable, small stemloop at the 3' end capable of forming a copyback structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP, and UTP nucleoside triphosphates (NTPs), where one of the NTP is a copyback structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP, and UTP nucleoside triphosphates (NTPs), where one of the NTP is a clivity of realplabelled and an assay buffer that supports replication activity of NS5B. The invention also relates to the identification of optimal properties of an RNA template for copy-back self-priming RNA synthesis of HCV. This activity can be used to screen for anti-HCV replicase compounds. The Characterise the biological relevance of lead compounds. The Optimal RNA templates can be used for developing a system to characterise the corpusation is useful for detecting HCV replicase activity. The nucleic acid synthesised by NS5B is detected by evaluating an autoradiograph of reaction products separated by gel electrophoresis. The present sequence is RNA template, A used to direct RNA synthesis by RNA polymerase proteins of the invention to the invention of the invention. 

0 T; 0 U; 0 Other; 34 A; 0 C; 2 G; BP; 36 Sequence

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                     Gaps
                     0;
       Length 36;
                     Indels
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             0.011;
     Score 33; DB 6;
Pred. No. 0.011,
0; Mismatches
                   0;
     1.6%;
ery Match
st Local Similarity 100.v
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Matches
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GAAAAAAAAAAAAAAAAAAAAAAAAA
      2066
           N
ò
          dd
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RESULT AAD271

AAD27117 standard; RNA;

ВP

36

(first entry) 09-APR-2002 AAD27117;

RNA synthesis by HCV RNA polymerase to direct AU used template, RNA

5B; NS5B; protein virus; HCV replicase; non-structural lead compound; RNA polymerase; ss Hepatitis C

Unidentified.

US6322966-B1

27-NOV-2001.

99US-00309670 11-MAY-1999; 99US-00309670. 11-MAY-1999;

ZHONG W. (ZHON/)

HONG Z. LAU J Y N. (LAUJ/) (HONG/)

Lau JYN; Hong Z, Zhong W,

2002-096587/13.

WPI;

Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates, buffer.

1A; 10pp; English. Fig Example 1;

The present invention relates to an assay system for hepatitis C virus

(HCV) replicase activity. The assay system comprises an RNA template that
has an unstable, small stemloop at the 3' end capable of forming a copyback structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
and UTP nucleoside triphosphates (NTPS), where one of the NTP is
radiolabelled and an assay buffer that supports replication activity of
NS5B. The invention also relates to the identification of optimal
reposerties of an RNA template for copy-back self-priming RNA synthesis of
HCV This activity can be used for developing a system to characterise
cort ocharacterise the biological relevance of lead compounds.
Cort ocharacterise the biological relevance of the activity.
HCV NS5B polymerase mechanistically and kinetically and for designing small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
system of the invention is useful for detecting HCV replicase activity.
The nucleic acid synthesised by NS5B is detected by evaluating an autoradiograph of reaction products separated by gel electrophoresis. The present sequence is RNA template, AU used to direct RNA synthesis by RNA
coplymerase proteins of HCV, BVDV and polivirus. This sequence is used in polymerase proteins of HCV, BVDV and the exemplification of the invention 

0 Other; Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U;

. 0 Length 36; Indels ö UB 6;
Lu. No. 0.011;
Mismatches Score 33; Pred. , o 1.6%; Similarity 100 33; Query Match Best Local Best Loc Matches

; 0

Gaps

2098 34 2066 СААДАДАДАДАДАДАДАДАДАДАДАДД ~

qq

Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

discrimination P1 primer #16.

Allele

olymerase

NS5B;

entry)

(first

14-FEB-2002

AAS95732

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The present invention relates to an assay system for hepatitis C virus (HCV) replicase activity. The assay system comprises an RNA template the has an unstable, small stemloop at the 3' end capable of forming a copy has an unstable, small stemloop at the 3' end capable of forming a copy back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP, and UTP nucleoside triphosphates (NTPS), where one of the NTP is radiolabelled and an assay buffer that supports replication activity of NS5B. The invention also relates to the identification of optimal properties of an RNA template for copy-back self-priming RNA synthesis or to characterise the biological relevance of lead compounds. The coptimal RNA templates can be used for developing a system to characterise the biological relevance of lead compounds. The optimal RNA molecules to co-crystallise with HCV NS5B polymerase. The assaystem of the invention is useful for detecting HCV replicase activity. The nucleic acid synthesised by NS5B is detected by evaluating an autoradiograph of reaction products separated by gel electrophoresis. The resent sequence is RNA template, (AU) 2 used to direct RNA synthesis by RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is un the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates,
                                                                                                                                                                            virus; HCV replicase; non-structural protein 5B;
                                                                                                                                         (AU) 2 used to direct RNA synthesis by HCV RNA
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                                                                                                                                                                                               lead compound; RNA polymerase; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 2A; 10pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lau JYN;
                                  37
                                                                                                        entry)
                                  standard; RNA;
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                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LAUJYN
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                                                                                                                                                                                                                                                                                                                                                                                                               ZHONG
HONG Z
                                                                                                                                             RNA template,
                                                                                                                                                                                                                                   Unidentified
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                                                                     AAD27125;
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RESULT 10
                   AAD271
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Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

STAGING INC

(MOLE-) MOLECULAR

ь;

Abarzua

WPI; 2002-049157/06.

2000US-0194843P

05-APR-2000;

2001WO-US011151

05-APR-2001;

18-OCT-2001

WO200177390-A2

Homo sapiens

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The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (PI) with a target contacting an allele-specific oligonucleotide primer (PI) with a target polynucleotide to form a hybridisation complex, where the target sequence is complementary to PI at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of PI may not be complex is then contacted with an exonuclease complexed by the the target DNA as the template, thereby forming an extended segment of PI. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3 ends, hence the absence of sequence amplification indicates the presence of a single the absence of sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obseity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and melanoma. Sequences AAS95711-AAS95745 represent primers, targets and fluorescence decorators used in the detection of RCA products
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illarity 100.0%;
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33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15;
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activity.

synthesis of ase compounds

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CTP,

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electrophoresis.

This sequence is

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46

AAS95736/c ID AAS95736 standard; DNA;

RESULT 12

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Gaps

0;

Indels

0;

Mismatches

..0

Conservative

Similarity 33; Conser

Query Match Best Local

Matches

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DB

Score 33; Pred. No.

1.6%;

2098

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2066

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RESULT 11 AAS95732/c ID AAS95732 standard; DNA; 46 BP

34

Length 37;

(first entry) 14-FEB-2002

discrimination Pl primer #20. Allele

stomach; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; Bs; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomachlung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe. amplification; Rolling circle

Homo

WO200177390-A2

18-OCT-2001

2001WO-US011151 05-APR-2001;

2000US-0194843P 05-APR-2000; (MOLE-) MOLECULAR STAGING INC.

<u>.</u> Abarzua 2002-049157/06.

otarget target amplifying t Detecting single nucleotide polymorphism involves amplifyin sequences using small primer probe that matches or mismatcl sequence and extending primer probe which is then detected

86; 139pp; English.

Disclosure; Page

Claim 15; Page 43; 67pp; English

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (PI) with a target contacting an allele-specific oligonucleotide primer (PI) with a target bolymucleotide to form a hybridisation complex, where the target sequence is complementary to PI at one end but the terminal nucleotide and the complementary. The complex is then contacted with an exonuclease complementary. The complex is then contacted with an exonuclease complementary. The complex is the template, thereby forming an extended of PI with the target DNA as the template, thereby forming an extended of PI with the target DNA as the template, thereby forming an extended of sequence anglification indicates the presence of a single polymucleotide mismatch. Primer sequences complementary to a sequence on an uncleotide mismatch. Primer sequences complementary to a sequence on an uncleotide mismatch. Primer sequences complementary to a sequence on an uncleotide mismatch in at least one gene, such as Parkinson's disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, human hreast colon overy teatie or novery teatie or novery teatie or novery teatie or novery teaties. decorators used in the detection of RCA products

The state of the sta cancers of the head, neck, skin, brain, oesophaguesast, colon, ovary, testis or prostate, leukaemia, Sequences AAS95711-AAS95745 represent primers, ta fluorescence melanoma. 

Sequence 46 BP;

Length 46; Indels 0; 9 red. No. 0.01; Mismatches DB Score 33; Pred .. O 1.6%; Conservative Similarity 33; Query Match Best Local S Matches 33

**САААААААААААААААААААААААА** 38

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standard; cDNA; AAV02146 13 RESULT 13
AAV02146
ID AAV0

49

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encoded clones present in ATCC 98026 - possibly
proliferation/differentiation regulating,
any other activities.
                                  portion including the polyA tail
                                                immunomodulation;
                                                                                                                                                 Merberg
                                               cytokine; in regulation;
                                                                                                                                                Lavallie ER,
                                             1. secreted protein; ATCC 98026;
proliferation; differentiation;
                                                                                                                                                                             New secreted proteins encoded clones having cytokine, cell proliferation/dimmunomodulating and many other activ
                                  3,
                                                                                                                                                ĽĀ,
                                 Human secreted protein AK533
                                                                                                                     96US-00634325
                                                                                                         97WO-US006139
                                                                                                                                                Racie
                    (first entry)
                                                                                                                                  GENETICS INST INC.
                                                                                                                                               Ğ,
                                                                                                                                                                  WPI; 1997-526460/48
                                                                                                                                               Mccoy
                                                                             WO9739123-A2
                                                                 Homo sapiens
                                                                                                       14-APR-1997;
                                                                                                                    18-APR-1996;
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,
                   12-MAY-1998
                                                                                           23-OCT-1997
                                                                                                                                                     Spaulding
                                                                                                                                               Jacobs K,
                                                                                                                                 (GEMY)
                                             Human;
                                                    cell
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The present sequence encodes a portion of a novel human secreted protein deposited under accession number ATCC 98026. The secreted protein can be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities although no evidence for any is provided in the specification. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating treating human immunodeficiency virus infection, cancer, autoimmune cytokines; immunostimulation of haematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation of growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, periodontal disease, neurological diseases stroke, fibrosis); inhibition or stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activity (e.g. for treating infections, tumours); haemostatic or thrombolytic activity (e.g. for treating control of fertility cartivity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating representation of the control of fertility control of for treating septic shock, Crohn's disease); as antimicrobials; for treating representation of the control of fertility treating septic shock, Crohn's disease); as antimicrobials; for treating for treating for treating for treating for treating for treating septic shock, crohn's disease); as antimicrobials; for treating f gulation or other hyperproliferative disease; for regulatic our, and many others. Also contemplated is the use nucleic acid in gene therapy procedures metabolism, behaviour, and the corresponding nucleic treating psoriasis metabolism, behavio behavi

6 G; 1 T; 0 U; 0 Other; Ċ; N Ą 40 49 BP; Sequence

Indels Length ; 0.01; N DB Mismatches Score 33; Pred. No. 100.0%; Pi 1.68; Conservative Similarity 33; Query Match Best Local S Matches 33

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Gaps

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Gaps

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2098

9

standard; cDNA; 49 BP AAT88080 RESULT 14

XXX

ID

AAT88080;

dв

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Human; secreted protein; research; treatment; AM533; 3' portion;
          clone encoding secreted protein AK533
                                                                                                                             and murine secreted proteins - useful in r
ses or disorders related to their function.
                                                                                                                                              140pp; English
                                                                                96US-00631184.
                                                                    97WO-US006042
entry)
                                                                                           MURO PHARM INC
                                                                                                                                              86;
                                                                                                                   WPI; 1997-526459/48.
                                                                                                                                                                                                                                                                                    49 BP; 40
                                                                                                                                                                                                                                                                                                    Similarity 33; Conser
(first
           CDNA
                                                                                                                                                Page
           of
                                   Homo sapiens
                                                                                                                                                                                                                                                                   and K35
FCM-4)
                                              WO9739122-A2
                                                                                 12-APR-1996;
                                                                                                                                                Disclosure;
                                                                                                        Theoharides
                                                          23-OCT-1997
                                                                     11-APR-1997
14-MAY-1998
           portion
                                                                                                                                                                                                                                                                                     Sequence
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Best Local
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                                                                                            (MURO-)
                                                                                                                               Human
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The present sequence is the 3' portion of a cDNA clone encoding a human secreted protein, which may have nutritional uses, or cytokine and cell proliferation/differentiation, immune stimulating or suppressing, haematopoiesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, anti-inflammatory or tumour inhibition activities. It can also be used to research or treat diseases/disorders related to its function. The partial cDNA clones AB931, AM610, AM340, AM282, AK647, library. The partial cDNA clones A617 and BB9 were 1st isolated from a human foetal kidney cDNA library. The partial cDNA clones H617 and BB9 were 1st isolated from a human ovary (PA-1) partial cDNA clones A1919 were 1st isolated from a human foetal brain cDNA library. The partial cDNA clones A334 and A332 were 1st isolated from a human foetal brain cDNA library. The partial cDNA clones A334 and A532 were 1st isolated from a human adult retina cDNA library. The partial cDNA clones A334 and A532 were 1st isolated from a human adult retina cDNA library. The partial cDNA clones A334 and A532 were 1st isolated from a human adult retina cDNA library. The partial cDNA clones A334 and A532 were 1st isolated from a murine bone marrow (stromal collection of the partial cDNA clones A334 and A332 were lones and cDNA clones A334 and A332 were lones a lones a lone marrow (stromal collection of the partial cDNA clone marrow (stromal collec
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26-MAY-1991
                                                       AAN70278;
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Synthetic

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100.0%;
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